

10/525365

DT01 Rec'd PCT/EP 23 FEB 2005

SEQUENCE LISTING

<110> RIKEN et al

<120> Chromo protein and fluorescent protein

<130> 35

<160> A31519A

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<211> 229

<212> PRT

<213> Anthopleura inornata

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Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly

35 40 45

Gly Pro Leu Pro Phe Ala Tyr Asp Thr Leu Thr Pro Cys Trp Met Tyr

50 55 60

Gly Ser Lys Thr Phe Ile Lys His Thr Ser Gly Ile Pro Asp Tyr Phe

65 70 75 80

Lys Glu Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr

85 90 95

Glu Asp Gly Gly Cys Leu Thr Ile His Gln Asp Thr Ser Met Gln Gly

100 105 110

Asp Cys Phe Ile Phe Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala

115	120	125
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130	135	140
Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met		
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Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr		
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Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe		
180	185	190
Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg		
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Arg Leu Gly His His		

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<212> DNA

<213> Anthopleura inornata

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Gly Ser Lys Thr Phe Ile Lys His Thr Ser Gly Ile Pro Asp Tyr Phe			
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aag gag tct ctt cct gaa ggc ttt act tgg gaa aga acg caa atc tac	288		
Lys Glu Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr			
85	90	95	
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Glu Asp Gly Gly Cys Leu Thr Ile His Gln Asp Thr Ser Met Gln Gly			
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Asp Cys Phe Ile Phe Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala			
115	120	125	
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145	150	155	160
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Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
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acc tac agg tcc aga aag gca gga caa aaa atg cca gag ttc cat ttc 576
Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe
180 185 190
ggg gat cat cgt att gag atc ctg aag gaa gaa gaa caa ggc atg cgt 624
Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg
195 200 205
att gaa caa tac gag gca gcg gtg gcg agg tac tgc gaa gct cca tcc 672
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Arg Leu Gly His His
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 Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 Lys Glu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr
 85 90 95
 Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly
 100 105 110
 Asp Cys Phe Ile Tyr Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala
 115 120 125
 Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val
 130 135 140
 Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met
 145 150 155 160
 Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
 165 170 175
 Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe
 180 185 190
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Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly
              35              40              45
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Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Ser Tyr
              50              55              60
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Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
      65              70              75              80
aag gag tcc ttc cct gaa ggc ttt act tgg gaa aga acg caa atc tac 288
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              85              90              95
gag gat gga ggc tct ctt tct att cac cag gac aca agc ctg cag gga 336
Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly
              100             105             110
gat tgt ttt att tac aag atc aaa gtc att ggc acc aac ttt cct gcc 384
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 130 135 140
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 145 150 155 160
 gcc ctg aaa tgc aag gat ggc aac cac ctg acg tgc cat ctg cga act 528
 Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
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 Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe
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 195 200 205
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<213> Trachyphyllia geoffroyi

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Pro	Phe	Glu	Gly	Lys	Gln	Ser	Met	Asp	Leu	Val	Val	Lys	Glu	Gly	Ala
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Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr	Gly
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					85					90					95
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									100					105	
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			130						135					140	
Lys	Met	Tyr	Leu	Arg	Asp	Gly	Val	Leu	Thr	Gly	Asp	Ile	Thr	Met	Ala
145					150					155					160
Leu	Leu	Leu	Lys	Gly	Asp	Val	His	Tyr	Arg	Cys	Asp	Phe	Arg	Thr	Thr
					165					170					175
Tyr	Lys	Ser	Arg	Gln	Glu	Gly	Val	Lys	Leu	Pro	Gly	Tyr	His	Phe	Val

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 cct ttt gag gga aaa cag agt atg gac ctt gta gtc aaa gaa ggc gca 144
 Pro Phe Glu Gly Lys Gln Ser Met Asp Leu Val Val Lys Glu Gly Ala
 35 40 45
 cct ctc cct ttt gcc tac gat atc ttg aca aca gca ttc cat tat ggt 192
 Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly
 50 55 60
 aac agg gtt ttt gct aaa tac cca gac cat ata cca gac tac ttc aag 240

aag ctg tat gag cat gct gtt gcc cat tct gga ttg ccg gac aac gtc 672

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220

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Lys

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<213> *Trachyphyllia geoffroyi*

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25

30

Pro Phe Glu Gly Lys Gln Ser Met Asp Leu Val Val Lys Glu Gly Ala

35

40

45

Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly

50

55

60

Asn Arg Val Phe Ala Lys Tyr Pro Asp His Ile Pro Asp Tyr Phe Lys

65

70

75

80

Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu

85

90

95

Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp

100

105

110

Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn
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 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu
 130 135 140
 Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Arg Met Glu
 145 150 155 160
 Leu Leu Leu Lys Gly Asp Val His Tyr Arg Cys Asp Phe Arg Thr Thr
 165 170 175
 Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val
 180 185 190
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 35 40 45
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 Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly
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 Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp
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Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro		
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Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr		
130	135	140
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met		
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Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr		
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Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe		
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Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn		
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Glu Lys Gln Gln Gln		
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Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly
          20           25           30
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Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
          35           40           45
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
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Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
          65           70           75           80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
          85           90           95
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly
          100          105          110
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 aat ggt cca gtt atg cag aag aag acg cag aaa tgg gag caa tcc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr
 130 135 140
 gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att aac atg 480
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met
 145 150 155 160
 gct ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac ttc aga act 528
 Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr
 165 170 175
 act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc tac cac ttt 576
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe
 180 185 190
 ata gat cac tgc ata gag att tta agc cat cgc aac gat tac aac aac 624
 Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn
 195 200 205
 gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac aaa 672
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35 40 45
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
50 55 60
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
65 70 75 80
Glu Gln Ser Phe Pro Lys Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
85 90 95
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Glu Gly
100 105 110
Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro
115 120 125
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Pro Ser Thr
130 135 140
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met
145 150 155 160
Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr

	165	170	175
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe			
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Ile Asp His Cys Ile Glu Ile Leu Ser His His Asn Asp Tyr Asn Asn			
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Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys			
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Glu Lys Gln Gln Gln			
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Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly
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Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
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Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro			
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	130	135	140
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Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met			
145	150	155	160
gct ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac ttc aga act 528			
Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr			
	165	170	175
act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc tac cac ttt 576			
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe			
	180	185	190
ata gat cac tgc ata gag att tta agc cat cac aac gat tac aac aac 624			

Ile Asp His Cys Ile Glu Ile Leu Ser His His Asn Asp Tyr Asn Asn
195 200 205
gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac aaa 672
Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys
210 215 220
gag aaa caa caa caa tga 690
Glu Lys Gln Gln Gln
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<213> Scolymia Vitiensis

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Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
50 55 60
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
65 70 75 80
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
85 90 95

Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly
 100 105 110
 Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro
 115 120 125
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr
 130 135 140
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asn Met
 145 150 155 160
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 165 170 175
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe
 180 185 190
 Ile Asp His Cys Met Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn
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 Glu Lys Gln Gln Gln
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<213> Scolymia Vitiensis

<400> 14

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Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly			
20	25	30	
aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144			
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly			
35	40	45	
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192			
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr			
50	55	60	
ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240			
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe			
65	70	75	80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288			
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe			
85	90	95	
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336			
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly			
100	105	110	
ggc act ttc tat aat aaa gtt cga ttt tat ggt gta aat ttc ccc ccc 384			
Gly Thr Phe Tyr Asn Lys Val Arg Phe Tyr Gly Val Asn Phe Pro Pro			
115	120	125	
aat ggt cca gtt atg cag aag aag acg cag aaa tgg gag caa tcc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Lys Trp Glu Gln Ser Thr			
130	135	140	
gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att aac atg 480			

20	25	30
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly		
35	40	45
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr		
50	55	60
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe		
65	70	75
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe		
	85	90
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly		
100	105	110
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Val Asn Phe Pro Pro		
115	120	125
Asn Gly Pro Val Met Gln Lys Asn Thr Leu Lys Trp Glu Pro Ser Thr		
130	135	140
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met		
145	150	155
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr		
	165	170
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr		
180	185	190
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn		
195	200	205
Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp		
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<210> 16

<211> 672

<212> DNA

<213> Scolymia Vitiensis

<400> 16

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ggc agt gta aac gga cac gac ttc gtg att gac gga act ggt tca ggc 96
Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Thr Gly Ser Gly
              20              25              30
aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
              35              40              45
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
              50              55              60
ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
              65              70              75              80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg att ttc 288
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ile Phe
              85              90              95
gaa gac ggg ggc att tgc atc gct aga aac gac ata aca atg gat ggt 336
Glu Asp Gly Gly Ile Cys Ile Ala Arg Asn Asp Ile Thr Met Asp Gly
              100             105             110
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ggc act ttc tat aat aaa gtt cga ttt gaa ggt gta aat ttc ccc ccc 384
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 115 120 125
 aat ggt cca gtt atg cag aag aat acg ctg aaa tgg gag cca tcc act 432
 Asn Gly Pro Val Met Gln Lys Asn Thr Leu Lys Trp Glu Pro Ser Thr
 130 135 140
 gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att gac atg 480
 Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met
 145 150 155 160
 tcc ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac ttc aga act 528
 Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr
 165 170 175
 act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc acc cac tac 576
 Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr
 180 185 190
 ata gat cac agc ata gag att tta agc cat cgc aac gat tac aac aac 624
 Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn
 195 200 205
 gtt acg ctt ttt gag cat gct gtt gct cgt tct gga ttg cag gac taa 672
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<210> 17

<211> 223

<212> PRT

<213> Scolymia Vitiensis

<400> 17

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35 40 45
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
50 55 60
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
65 70 75 80
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Thr Phe
85 90 95
Glu Asp Gly Gly Val Cys Thr Ala Arg Asn Asp Ile Thr Met Asp Gly
100 105 110
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Thr Asn Phe Pro Pro
115 120 125
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr
130 135 140
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met
145 150 155 160
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Met Arg Thr
165 170 175
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr
180 185 190
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn

195	200	205
Val Thr Leu Tyr Glu His Ala	Val Ala Arg Ser Gly Leu Gln Asp	
210	215	220

<210> 18

<211> 672

<212> DNA

<213> Scolymia Vitiensis

<400> 18

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Met Val Ser Val Ile Lys Asp Glu Met Lys Val Arg Leu Arg Met Glu
      1              5              10              15
ggc agt gta aac gga cac gac ttc gtg att gac gga act ggt tca ggc 96
Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Thr Gly Ser Gly
              20              25              30
aag cct aaa gag gga aca cag act att gag ctt aaa gtc gta aag ggt 144
Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
              35              40              45
gga cct tta cct ttc gcc tac gat atc ctg aca aca gca ttc cat tac 192
Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr
              50              55              60
ggc aac cgg gta ttc gcc aaa tac cca aag gat ata cca aac tat ttc 240
Gly Asn Arg Val Phe Ala Lys Tyr Pro Lys Asp Ile Pro Asn Tyr Phe
      65              70              75              80
gag cag tcg ttt cct gag ggg tat tcg tgg gaa cgg agc atg act ttc 288
Glu Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Thr Phe

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85	90	95	
gaa gac ggg ggc gtt tgc acc gct aga aac gac ata aca atg gat ggt 336			
Glu Asp Gly Gly Val Cys Thr Ala Arg Asn Asp Ile Thr Met Asp Gly			
100	105	110	
ggc act ttc tat aat aaa gtt cga ttt gaa ggt aca aat ttc ccc ccc 384			
Gly Thr Phe Tyr Asn Lys Val Arg Phe Glu Gly Thr Asn Phe Pro Pro			
115	120	125	
aat ggt cca gtt atg cag aag aag acg ctg aaa tgg gag cca tcc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr			
130	135	140	
gag aaa atg tat gcg cgt gat gga gtg ttg acg ggt gat att gac atg 480			
Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Thr Gly Asp Ile Asp Met			
145	150	155	160
tcc ctg ttg ctt aaa ggg ggt ggc cat tac cga tgt gac atg aga act 528			
Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Met Arg Thr			
165	170	175	
act ttc aaa gct aag gag aag ggt gtc aag ttg cca ggc acc cac tac 576			
Thr Phe Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Thr His Tyr			
180	185	190	
ata gat cac agc ata gag att tta agc cat cgc aac gat tac aac aac 624			
Ile Asp His Ser Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn			
195	200	205	
gtt acg ctt tat gag cat gct gtt gct cgt tct gga ttg cag gac taa 672			
Val Thr Leu Tyr Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp			
210	215	220	

<210> 19

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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acvggdccat ydgvaagaaa rtt 23

<210> 21

<211> 36

<212> DNA

<213> Artificial Sequence

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<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 23

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ggccacgcgt cgactagtac 20

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 24

aaaatatcgt acgcaaaggg 20

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<400> 25

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<210> 26

<211> 33

<212> DNA

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<210> 27

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<223> Description of Artificial Sequence: Synthetic DNA

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<223> Description of Artificial Sequence: Synthetic DNA

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acvggdccat ydgvaagaaa rtt 23

<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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agttcacacc atgatattca atatcata 28

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 31

ggccacgcgt cgactagtac 20

<210> 32

<211> 23

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 32

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<210> 33

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<223> Description of Artificial Sequence: Synthetic DNA

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 35

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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ccgctcgagt tgttgttggtt tctctttgtc ctg

33